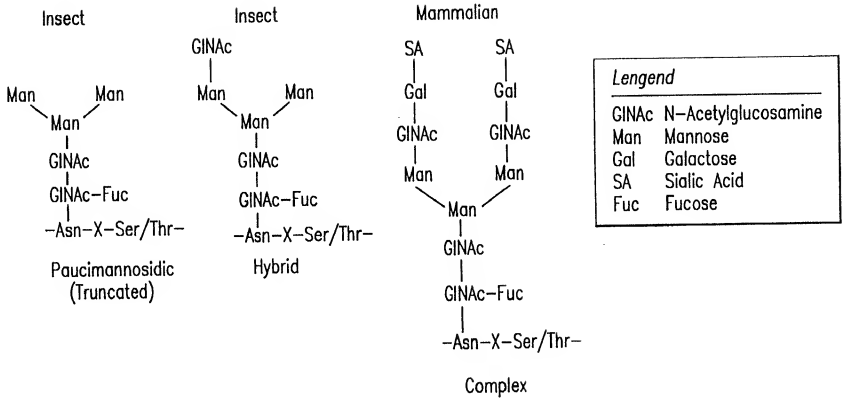


FIG.1

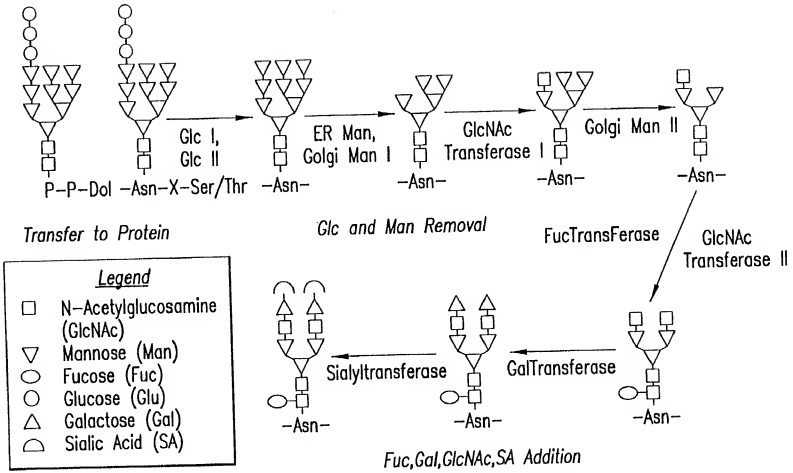


FIG.2

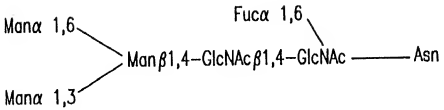


FIG.3

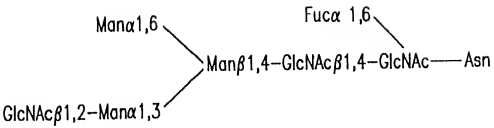


FIG.4A

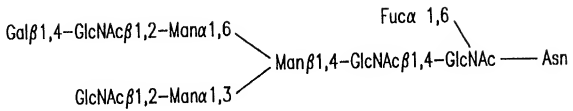


FIG.4B

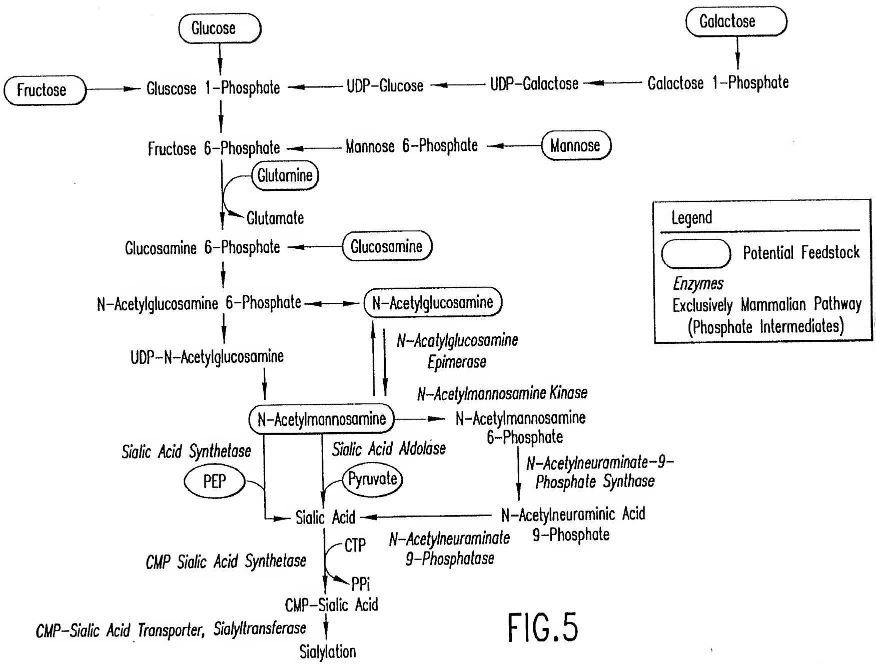

Glucose
Galactose
Fructose
Gluscose 1–Phosphate
UDP–Glucose
UDP–Galactose
Galactose 1–Phosphate
Fructose 6–Phosphate
Mannose 6–Phosphate
Mannose
Glutamine
Glutamate
Glucosamine 6–Phosphate
Glucosamine
N–Acetylglucosamine 6–Phosphate
N–Acetylglucosamine
UDP–N–Acetylglucosamine
N–Acatylglucosamine Epimerase
N–Acetylmannosamine Kinase
N–Acetylmannosamine
N–Acetylmannosamine 6–Phosphate
Sialic Acid Synthetase
Sialic Acid Aldolase
N–Acetylneuraminate–9–Phosphate Synthase
PEP
Pyruvate
Sialic Acid
N–Acetylneuraminic Acid 9–Phosphate
CTP
N–Acetylneuraminate 9–Phosphatase
CMP Sialic Acid Synthetase
PPi
CMP–Sialic Acid
CMP–Sialic Acid Transporter, Sialyltransferase
Sialylation
Legend
Potential Feedstock
Enzymes
Exclusively Mammalian Pathway (Phosphate Intermediates)

FIG.5

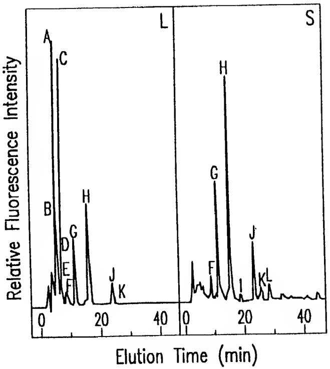

Relative Fluorescence Intensity
L
S
A
B
C
D
E
F
G
H
I
J
K
L
0
20
40
Elution Time (min)

FIG.6

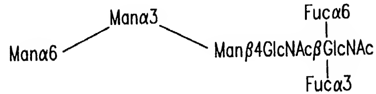

Manα6
Manα3
Manβ4GlcNAcβGlcNAc
Fucα6
Fucα3

FIG.7

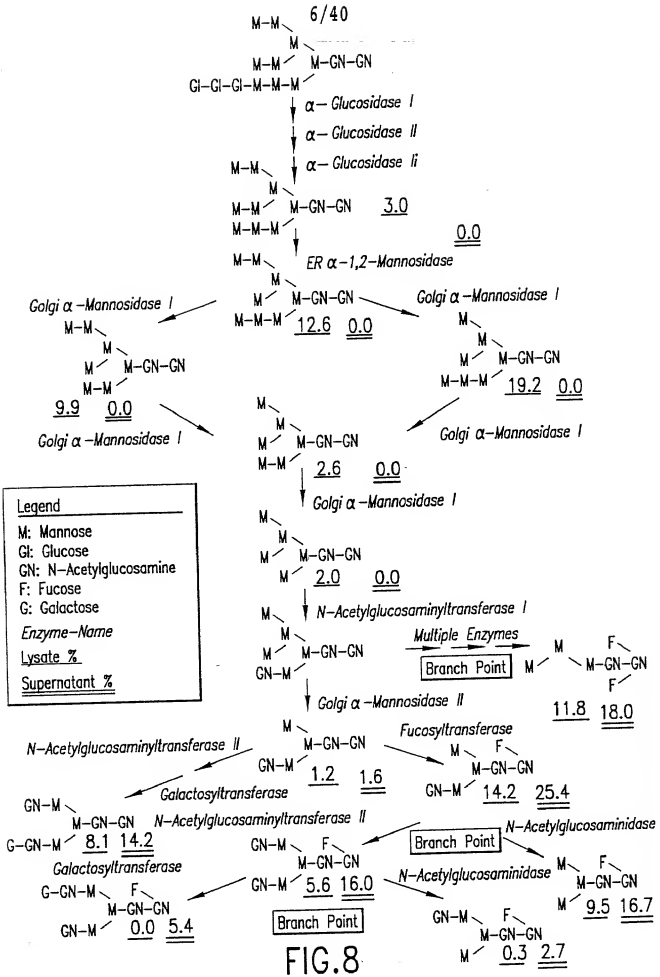

M-M
M
M-M
M-GN-GN
Gl-Gl-Gl-M-M-M
α– Glucosidase I
α– Glucosidase II
α– Glucosidase Ii
3.0
0.0
ER α–1,2–Mannosidase
Golgi α –Mannosidase I
12.6 0.0
19.2 0.0
9.9 0.0
2.6 0.0
2.0 0.0
N–Acetylglucosaminyltransferase I
Multiple Enzymes
Branch Point
11.8 18.0
Golgi α –Mannosidase II
Fucosyltransferase
N–Acetylglucosaminyltransferase II
1.2 1.6
14.2 25.4
Galactosyltransferase
8.1 14.2
5.6 16.0
N–Acetylglucosaminidase
9.5 16.7
0.0 5.4
0.3 2.7
Legend
M: Mannose
Gl: Glucose
GN: N–Acetylglucosamine
F: Fucose
G: Galactose
Enzyme–Name
Lysate %
Supernatant %

FIG.8

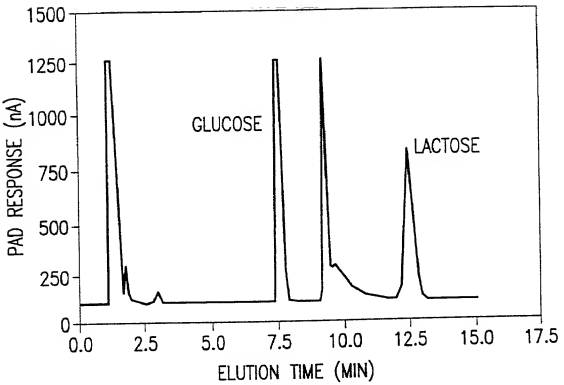

1500
1250
1000
750
500
250
0
PAD RESPONSE (nA)
GLUCOSE
LACTOSE
0.0
2.5
5.0
7.5
10.0
12.5
15.0
17.5
ELUTION TIME (MIN)

FIG. 9

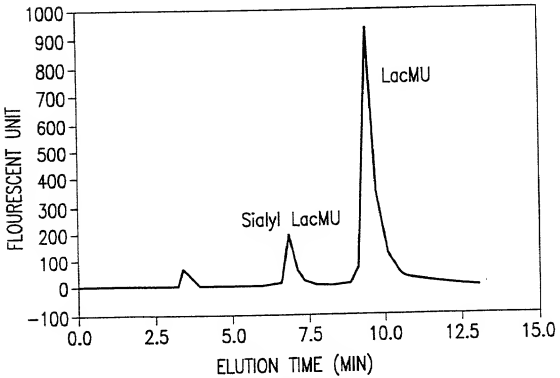

1000
900
800
700
600
500
400
300
200
100
0
-100
FLOURESCENT UNIT
LacMU
Sialyl LacMU
0.0
2.5
5.0
7.5
10.0
12.5
15.0
ELUTION TIME (MIN)

FIG. 10

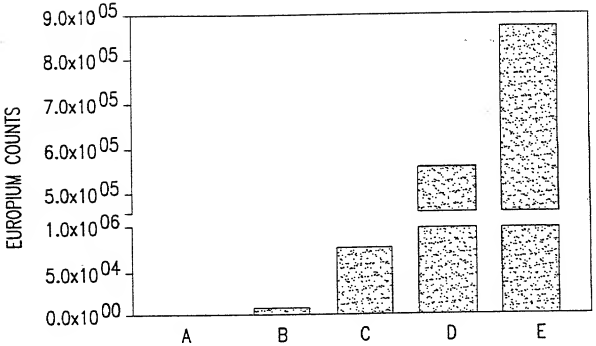
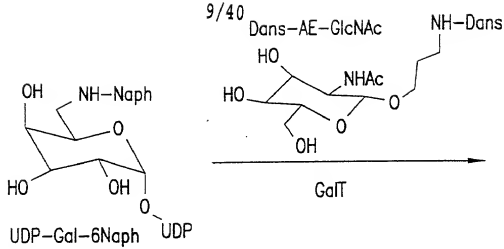

EUROPIUM COUNTS
9.0x10 05
8.0x10 05
7.0x10 05
6.0x10 05
5.0x10 05
1.0x10 06
5.0x10 04
0.0x10 00
A
B
C
D
E

FIG. 11


Dans–AE–GlcNAc
NH–Dans
HO
NHAc
HO
O
O
OH
GalT
OH
NH–Naph
O
HO
OH
O
UDP
UDP–Gal–6Naph

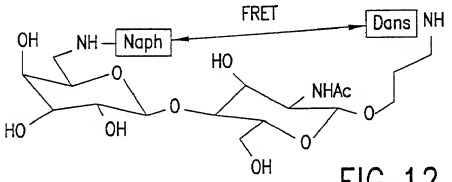

FRET
OH
NH
Naph
Dans
NH
HO
NHAc
O
HO
OH
O
OH

FIG. 12

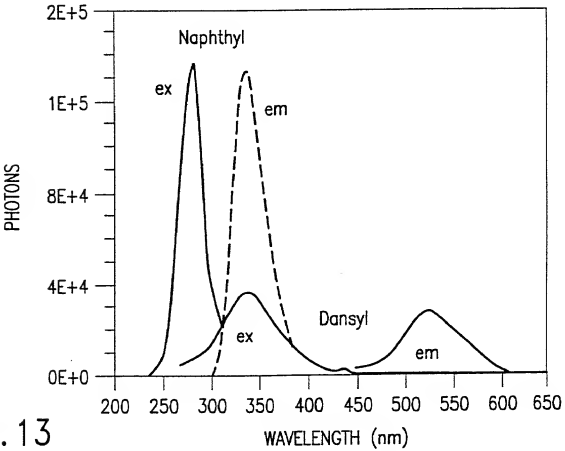

2E+5
1E+5
8E+4
4E+4
0E+0
PHOTONS
Naphthyl
ex
em
ex
Dansyl
em
200
250
300
350
400
450
500
550
600
650
WAVELENGTH (nm)

FIG. 13

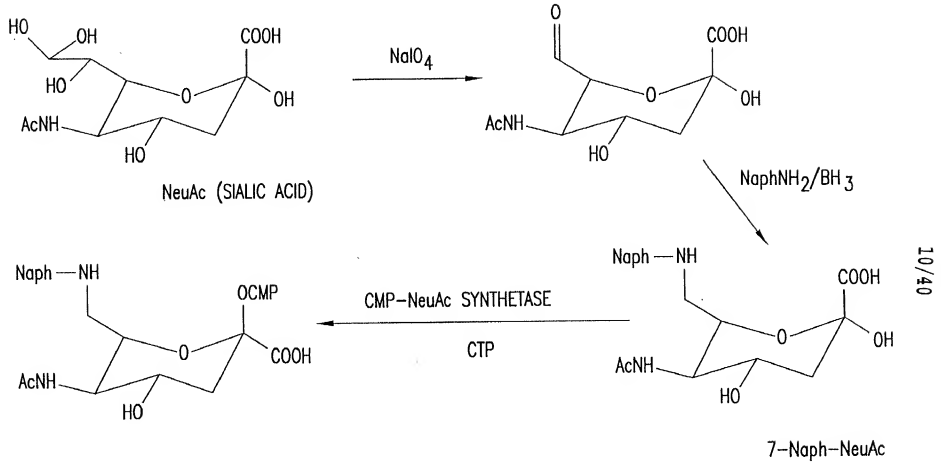


FIG. 14

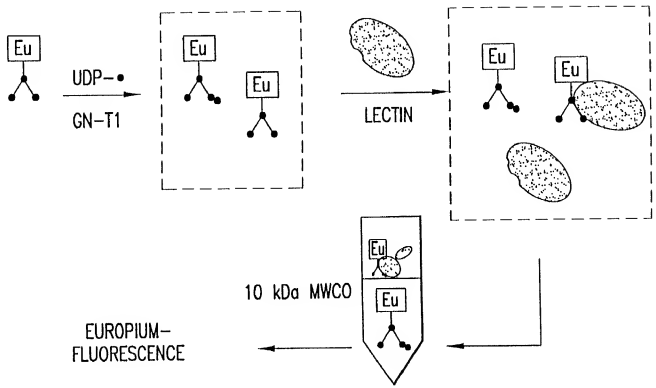

Eu
UDP-•
GN-T1
Eu
Eu
LECTIN
Eu
Eu
Eu
Eu
10 kDa MWCO
EUROPIUM-
FLUORESCENCE

FIG. 15

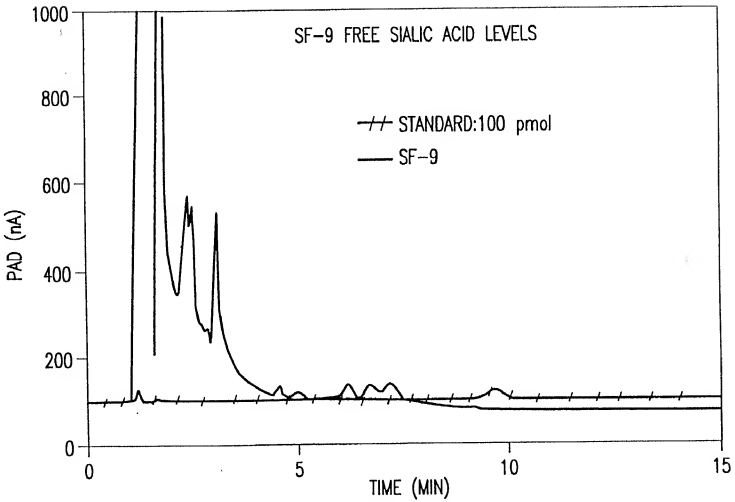

SF-9 FREE SIALIC ACID LEVELS
STANDARD:100 pmol
SF-9
PAD (nA)
TIME (MIN)
1000
800
600
400
200
0
0
5
10
15

FIG.16A

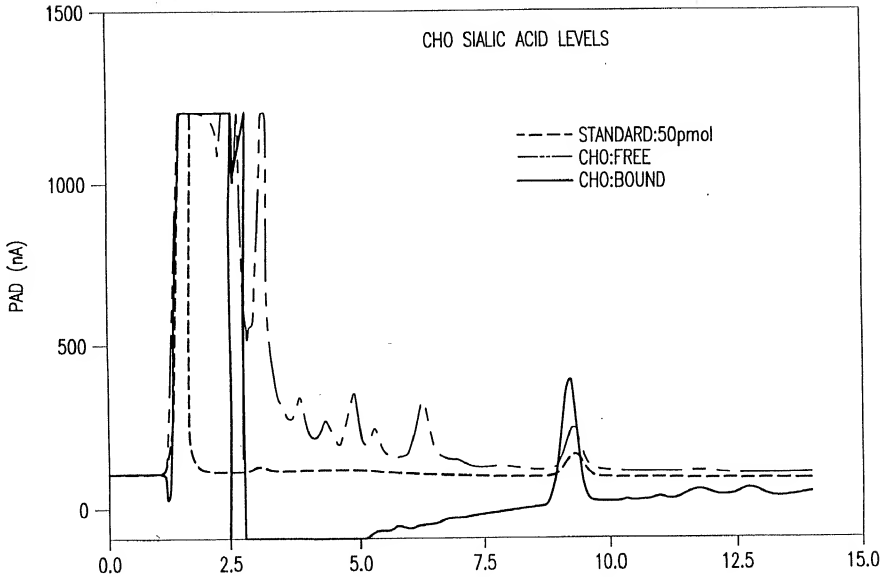


FIG.16B

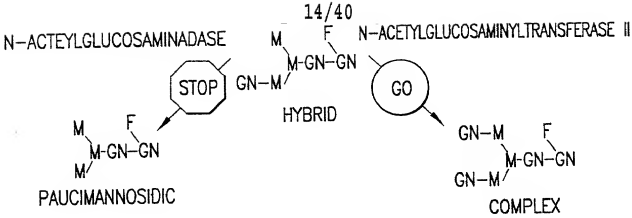
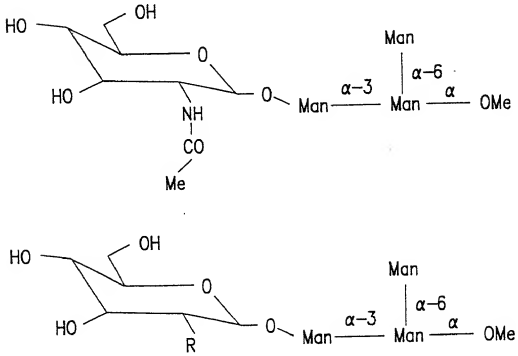


FIG. 17



R=MeCONH I I
R=BrCH$_2$CONH III
R=N$_2$CH$_2$CONH IV

FIG. 19

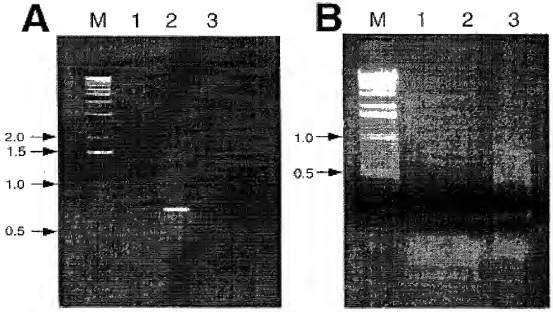


FIG. 18A FIG. 18B

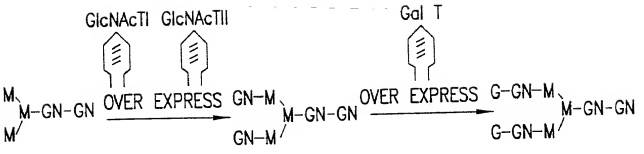


FIG. 20

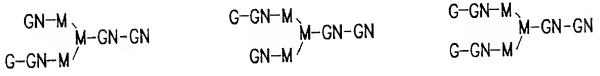


FIG. 21

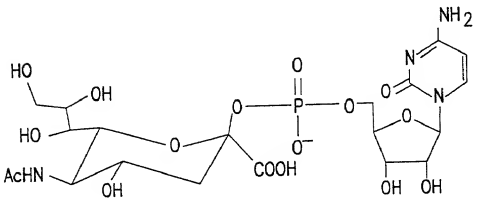


FIG. 22

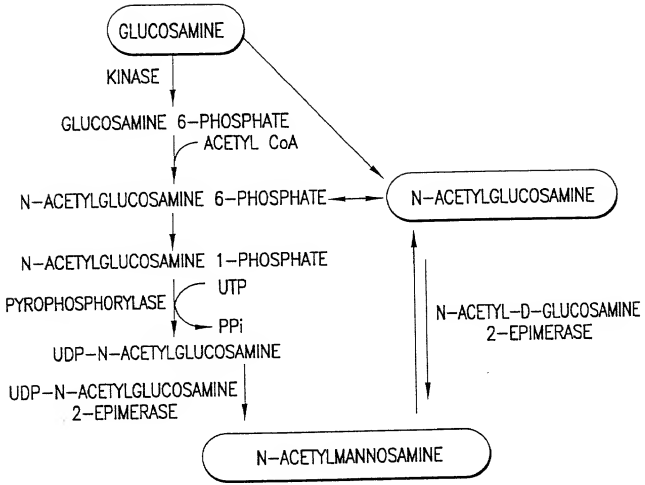

GLUCOSAMINE
KINASE
GLUCOSAMINE 6-PHOSPHATE
ACETYL CoA
N-ACETYLGLUCOSAMINE 6-PHOSPHATE
N-ACETYLGLUCOSAMINE
N-ACETYLGLUCOSAMINE 1-PHOSPHATE
PYROPHOSPHORYLASE
UTP
PPi
UDP-N-ACETYLGLUCOSAMINE
UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE
N-ACETYL-D-GLUCOSAMINE 2-EPIMERASE
N-ACETYLMANNOSAMINE

FIG. 23

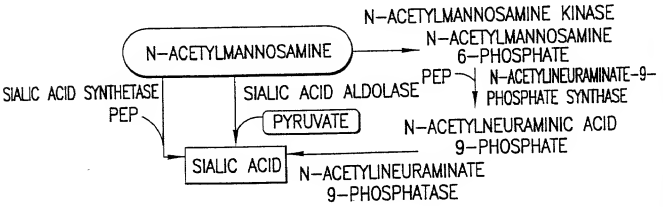

N-ACETYLMANNOSAMINE KINASE
N-ACETYLMANNOSAMINE
N-ACETYLMANNOSAMINE 6-PHOSPHATE
PEP
N-ACETYLNEURAMINATE-9-PHOSPHATE SYNTHASE
SIALIC ACID SYNTHETASE
PEP
SIALIC ACID ALDOLASE
PYRUVATE
N-ACETYLNEURAMINIC ACID 9-PHOSPHATE
SIALIC ACID
N-ACETYLNEURAMINATE 9-PHOSPHATASE

FIG. 24

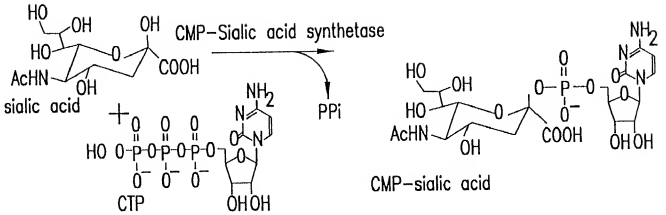


FIG.25

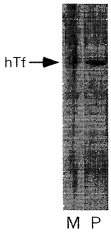


FIG. 26

ATGGCCTTCCCAAAGAAGAAACTTCAGGGTCTTGTGGCTGCAACCATCACGCCAATGACTGAGAATGGAGAAATCAA
CTTTTCAGTAATTGGTCAGTATGTGGATTATCTTGTGAAAGAACAGGGAGTGAAGAACATTTTTGTGAATGGCACAA
CAGGAGAAGGCCTGTCCCTGAGCGTCTCAGAGCGTCGCCAGGTTGCAGAGGAGTGGGTGACAAAAGGGAAGCACAAG
CTGGATCAGGTGATAATTCACGTAGGAGCACTGAGCTTGAAGGAGTCACAGGAACTGGCCCAACATGCAGCAGAAAT
AGGAGCTGATGGCATCGCTGTCATTGCACCGTTCTTCCTCAAGCCATGGACCAAAGATATCCTGATTAATTTCCTAA
AGGAAGTGGCTGCTGCCGCCCCTGCCCTGCCATTTTATTACTATCACATTCCTGCCTTGACAGGGGTAAAGATTCGT
GCTGAGGAGTTGTTGGATGGGATTCTGGATAAGATCCCCACCTTCCAAGGGCTGAAATTCAGTGATACAGATCTCTT
AGACTTCGGGCAATGTGTTGATCAGAATCGCCAGCAACAGTTTGCTTTCCTTTTTGGGGTGGATGAGCAACTGTTGA
GTGCTCTGGTGATGGGAGCAACTGGAGCAGTGGGCAGTTTTGTATCCAGAGATTTATCAACTTTGTTGTCAAACTAG
GTTTTGGAGTGTCACAGACCAAAGCCATCATGACTCTGGTCTCTGGGATTCCAATGGGCCCACCCCGGCTTCCACTG
CAGAAAGCCTCCAGGGAGTTTACTGATAGTGCTGAAGCTAAACTGAAGAGCCTGGATTTCCTTTCTTTCACTGATTT
AAAGGATGGAAACTTGGAAGCTGGTAGCTAGTGCCTCTCTATCAAATCAGGGTTTGCACCTTGAGACATAATCTACC
TTAAATAGTGCATTTTTTTCTCAGGGAATTTTAGATGAACTTGAATAAACTCTCCTAGCAAATGAAATCTCACAATA
AGCATTGAGGTACCTTTTGTGAGCCTTAAAAAGTCTTATTTTGTGAAGGGCAAAAACTCTAGGAGTCACAACTCTC
AGTCATTCATTTCACAGATTTTTTTGTGGAGAAATTTCTGTTTATATGGATGAAATGGAATCAAGAGGAAAATTGTA
ATTGATTAATTCCATCTGTCTTTAGGAGCTCTCATTATCTCGGTCTCTGGTTCCTAATCCTATTTTAAAGTTGTCTA
ATTTTAAACCACTATAATATGTCTTCATTTTAATAAATATTCATTTGGAATCTAGGAAAACTCTGAGCTACTGCATT
TAGGCAGGCACTTTAATACCAAACTGTAACATGTCTCAACTGTATACAACTCAAAATACACCAGCTCATTTGGCTGC
TCAGTCTAACTCTAGAATGGATGCTTTTGAATTCATTTCGATG

FIG.27

MAFPKKKLQGLVAATITPMTENGEINFSVIGQYVDYLVKEQGVKNIFVNGTTGEGLSLSVSERRQVAEEWVTKGKDKLDQ
VIIHVGALSLKESQELAQHAAEIGADGIAVIAPFFLKPWTKDILINFLKEVAAAAPALPFYYYHIPALTGVKIRAEELLD
GILDKIPTFQGLKFSDTDLLDFGQCVDQNRQQQFAFLFGVDEQLLSALVMGATGAVGSFVSRDLSTLLSN.VLECHRPKP
S.LWSLGFQWAHPGFHCRKPPGSLLIVLKLN.RAWISFLSLI.RMETWKLVASASLSNQGFAPLRHNL

FIG.28

ATGGACTCGGTGCAGAAGGGGCCGCCACCTCCGTCTCCAACCGCGGGGGCGACCGTCCCGGGCCGGCCGCCGAAGCT
GCAGCGCAACTCTCGCCGGCGGCCAGGGCCGAGGTGTGGAGAAGCCCCCGCACCTGGCAGCCCTAATTCTGGCCCGGGGAG
GCAGCAAAGGCATCCCCCTGAAGAACATTAAGCACCTGGCCGGGGGTCCCGCTCATTGGCTGGGTCCTGCGTGCGGCCCTG
GATTCAGGGGCCTTCCAGAGTGTATGGGTTTCGACAGACCATGATGAAATTGAGAATGTGGCCAAACAATTTGGTGCACA
AGTTCATCGAAGAAGTTCTGAAGTTTCAAAAGACAGCTCTACCTCACTAGATGCCATCATAGAATTTCTTAATTATYATA
ATGAGGKTGACATTGTAGGAAATATTCAAGCTACTTCTYCATGTTTACATCCTACTGATCTTCAAAAAGTTGCAGAAATG
ATTCGAGAACAAGCATATGATTCTGKTTTCTCTGTTGTGAGACGCCATCAGTTTCGATGGAGTGAAATTCAGAAAGGAGT
TCGTGAAGTGACCGAACCTCTGAATTTAAATCCAGCTAAACGGCCTCGTCGACAAGACTGGGATGGAGAATTATATGAAA
ATGGCTCATTTTATTTTGCTAAAAGACATTTGATAGAGATGGGTTACTTGCAGGGTGCAAAATGGCATACTACGAAATGC
GAGCTGGAACATAGTGTGGATATAGATGTGGATATTGATTGGCCTATTGCAGAGCAAAGAGTATTAAGATATGGCTATTT
TGGCAAAGAGAAGCTTAAGGAAATAAAACTTTTGGTTTGCAATATTGATGGATGTCTCACCAATGGCCACATTTATGTAT
CAGGAGACCAAAAAGAAATAATATCTTATGATGTAAAAGATGCTATTGGGATAAGTTTATTAAAGAAAAGTGGTATTGAG
GTGAGGCTAATCTCAGAAAGGGCCTGTTCAAAGCAGACCCTGTCTTCTTTAAAACTGGATTGCAAAATGGAAGTCAGTGT
ATCAGACAAGCTAGCAGTTGTAGATGAATGGAGAAAAGAAATGGGCCTGTGCTGGAAAGAAGTGGCATATCTTGGAAATG
AAGTGTCTGATGAAGAGTGCTTGAAGAGAGTGGGCCTAAGTGGCGCTCCTGCTGATGCCTGTTCCTACGCCCAGAAGGCT
GTTGGATACATTTGCAAATGTAATGCTGGCCGTGGTGCCATCCGAGAATTTGCAGAGCACATTTGCCTACTAATGGAAAA
AGTTAATAATTCATGCCAAAAATAG

FIG.29

MDSVEKGAATSVSNPRGRPSRGRPPKLQRNSRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGWVLRAAL
DSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKDSSTSLDAIIEFLNYXNEXDIVGNIQATSXCLHPTDLQKVAEM
IREEGYDSXFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQDWDGELYENGSFYFAKRHLIEMGYLQGGKWHTTKC
ELEHSVDIDVDIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVSGDQKEIISYDVKDAIGISLLKKSGIE
VRLISERACSKQTLSSLKLDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLKRVGLSGAPADACSYAQKA
VGYICKCNGGRGAIREFAEHICLLMEKVNNSCQK.

FIG.30

ATGCCGCTGGAGCTGGAGCTGTGTCCCGGCGCTGGGTGGGCGGGCAACACCCGTGCTTCATCATTGCCGAGATCGGCCA
GAACCACCAGGGCGACCTGGACGTAGCCAAGCGCATGATCCCCATGGCCAAGGAGTGTGGGGCTGATTGTGCCAAGTTCC
AGAAGAGTGAGCTAGAATTCAAGTTTAATCGGAAAGCCTTGGAGAGGCCATACACCTCGAAGCATTCCTGGGGGAAGACG
TACGGGGAGCACAAACGACATCTGGAGTTCAGCCATGACCAGTACAGGGAGCTGCAGAGGTACGCCGAGGAGGTTGGGAT
CTTCTTCACTGCCTCTGGCATGGATGAGATGGCAGTTGAATTCCTGCATGAACTGAATGTTCCATTTTTCAAAGTTGGAT
CTGGAGACACTAATAATTTTCCTTATCTGGAAAAGACAGCCAAAAAAGGTCGCCCAATGGTGATCTCCAGTGGGATGCAG
TCAATGGACACCATGAAGCAAGTTTATCAGATCGTGAAGCCCCTCAACCCCAACTTCTGCTTCTTGCAGTGTACCAGCGC
ATACCCGCTCCAGCCTGAGGACGTCAACCTGCCGGTCATCTCGGAATATCAGAAGCTCTTTCCTGACATTCCCATAGGGT
ATTCTGGGCATGAAACAGGCATAGCGATATCTGTGGCCGCAGTGGCTCTGGGGGCCAAGGTGTTGGAACGTCACATAACT
TTGGACAAGACCTGGAAGGGGAGTGACCACTCCGCCTCGCTGGAGCCTGGAGAACTGGCCGAGCTGGTGCGGTCAGTGCG
TCTTGTGGAGCGTGCCCTGGGCTCCCCAACCAAGCAGCTGCTGCCCTGTGAGATGGCCTGCAATGAGAAGCTGGGCAAGT
CTGTGGTGGCCAAAGTGAAAATTCCGGAAGGCACCATTCTAACAATGGACATGCTCACCGTGAAGGTGGGTGAGCCCAAA
GCCTATCCTCCTGAAGACATCTTTAATCTAGTGCGCAAGAAGGTCCTGGTCACTGTTGAAGAGGATGACACCATCATGGA
AGAATTGGTAGATAATCATGGCAAAAAAATCAAGTCTTAA

FIG.31

MPLELELCPGRWVGGQHPCFIIAEIGQNHQGDLDVAKRMIRMAKECGADCAKFQKSELEFKFNRKALERPYTSKHSWGKT
YGEHKRHLEFSHDQYRELQRYAEEVGIFFTASGMDEMAVEFLHELNVPFFKVGSGDTNNFPYLEKTAKKGRPMVISSGMQ
SMDTMKQVYQIVKPLNPNFCFLQCTSAYPLQPEDVNLRVISEYQKLFPDIPIGYSGHETGIAISVAAVALGAKVLERHIT
LDKTWKGSDHSASLEPGELAELVRSVRLVERALGSPTKQLLPCEMACNEKLGKSVVAKVKIPEGTILTMDMLTVKVGEPK
AYPPEDIFNLVGKKVLVTVEEDDTIMEELVDNHGKKIKS

FIG.32

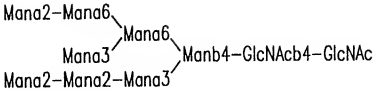
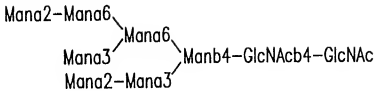
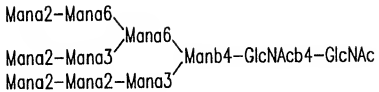
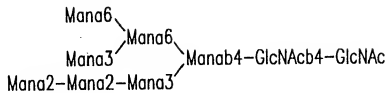
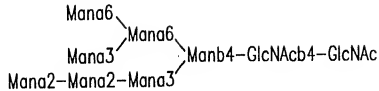
Peak/code (G.U. ODS, amide)	PA-oligosaccharide structure	Secreted hTf (mol%) -GalT	+GalT
A/M8.1 (4.9,9.0)		3.9	10.1
B1/M7.2 (5.1,8.1)		2.3	5.5
B2/M9.1 (5.2,9.7)		11.6	23.5
C/M7.1 (5.8,8.0)		2.3	5.5
D/M6.1 (6.1,7.1)		4.7	13.4

FIG.33A

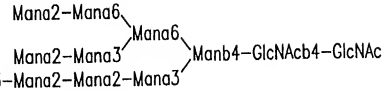
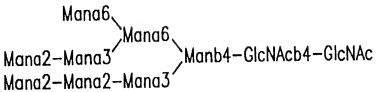
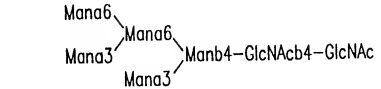
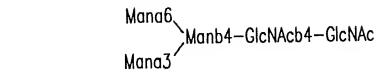
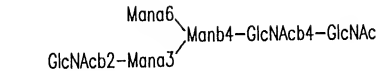
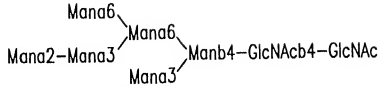
Peak/code (G.U. ODS, amide)	PA-oligosaccharide structure	Secreted hTf (mol%) -GalT	+GalT
E1/M9.2 (6.3,10.3)		1.3	3.7
E2/M8.2 (6.4,8.5)		0.3	0.8
F1/M5.1 (7.2,6.2)		4.6	2.4
F2/000.1 (7.4,4.3)		9.0	5.8
F3/100.2 (7.4,4.7)		6.5	3.1
G1/M6.10 (7.9,6.8)		1.1	1.1

FIG.33B

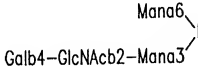
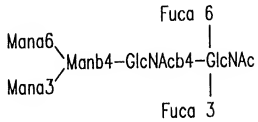
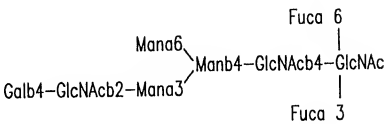
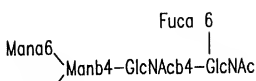
Peak/code (G.U. ODS, amide)	PA-oligosaccharide structure	Secreted hTf (mol%) -GalT	+GalT
G2/100.4 (8.0,5.7)		nd	5.0
H/000.1FF (8.5,5.5)		5.9	1.7
I/100.4FF (8.9,7.0)		nd	1.3
J1/010.0 (7.2,6.2)		23.4	4.0
J2/010.1 10.2,4.7)		15.7	6.1

FIG.33C

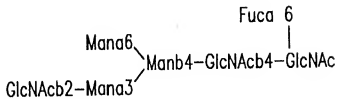
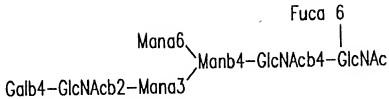
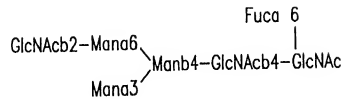
Peak/code (G.U. ODS, amide)	PA–oligosaccharide structure	Secreted hTf (mol%) –GalT	Secreted hTf (mol%) +GalT
J3/110.2 (10.2,5.1)		3.5	nd
K/110.4 (10.9,6.3)		nd	4.3
L/110.1 (12.7,5.1)		3.9	0.7

FIG.33D

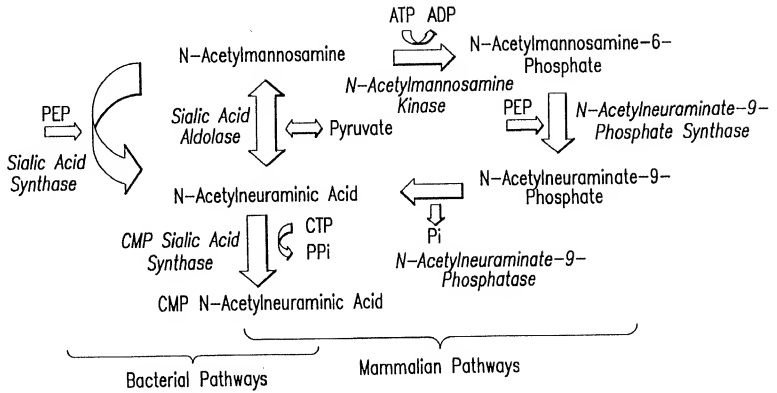


FIG.34

```
                10          20          30          40          50          60
                .           .           .           .           .           .
 1 CGG ACC CAG ACT GGT AGT GCA GGC TTT GGA CCC CGA GCC GCT GCA ATG CCG CTG GAG CTG 60
 1                                                                 M   P   L   E   L  5
                70          80          90          100         110         120
                .           .           .           .           .           .
61 GAG CTG TGT CCC GGG CGC TGG GTG GGC GGG CAA CAC CCG TGC TTC ATC ATT GCC GAG ATC 120
 6  E   L   C   P   G   R   W   V   G   G   Q   H   P   C   F   I   I   A   E   I 25
               130         140         150         160         170         180
                .           .           .           .           .           .
121 GGC CAG AAC CAC CAG GGC GAC CTG GAC GTA GCC AAG CGC ATG ATC CGC ATG GCC AAG GAG 180
 26  G   Q   N   H   Q   G   D   L   D   V   A   K   R   M   I   R   M   A   K   E 45
               190         200         210         220         230         240
                .           .           .           .           .           .
181 TGT GGG GCT GAT TGT GCC AAG TTC CAG AAG AGT GAG CTA GAA TTC AAG TTT AAT CGG AAA 240
 46  C   G   A   D   C   A   K   F   Q   K   S   E   L   E   F   K   F   N   R   K 65
               250         260         270         280         290         300
                .           .           .           .           .           .
241 GCC TTG GAG AGG CCA TAC ACC TCG AAG CAT TCC TGG GGG AAG ACG TAC GGG GAG CAC AAA 300
 66  A   L   E   R   P   Y   T   S   K   H   S   W   G   K   T   Y   G   E   H   K 85
               310         320         330         340         350         360
                .           .           .           .           .           .
301 CGA CAT CTG GAG TTC AGC CAT GAC CAG TAC AGG GAG CTG CAG AGG TAC GCC GAG GAG GTT 360
 86  R   H   L   E   F   S   H   D   Q   Y   R   E   L   Q   R   Y   A   E   E   V 105
               370         380         390         400         410         420
                .           .           .           .           .           .
361 GGG ATC TTC TTC ACT GCC TCT GGC ATG GAT GAG ATG GCA GTT GAA TTC CTG CAT GAA CTG 420
106  G   I   F   F   T   A   S   G   M   D   E   M   A   V   E   F   L   H   E   L 125
               430         440         450         460         470         480
                .           .           .           .           .           .
421 AAT GTT CCA TTT TTC AAA GTT GGA TCT GGA GAC ACT AAT AAT TTT CCT TAT CTG GAA AAG 480
126  N   V   P   F   F   K   V   G   S   G   D   T   N   N   F   P   Y   L   E   K 145
```

FIG. 35A

```
                490         500         510         520         530         540
                 .           .           .           .           .           .
481 ACA GCC AAA AAA GGT CGC CCA ATG GTG ATC TCC AGT GGG ATG CAG TCA ATG GAC ACC ATG 540
146 T   A   K   K   G   R   P   M   V   I   S   S   G   M   Q   S   M   D   T   M 165
                550         560         570         580         590         600
                 .           .           .           .           .           .
541 AAG CAA GTT TAT CAG ATC GTG AAG CCC CTC AAC CCC AAC TTC TGC TTC TTG CAG TGT ACC 600
166 K   Q   V   Y   Q   I   V   K   P   L   N   P   N   F   C   F   L   Q   C   T 185
                610         620         630         640         650         660
                 .           .           .           .           .           .
601 AGC GCA TAC CCG CTC CAG CCT GAG GAC GTC AAC CTG CGG GTC ATC TCG GAA TAT CAG AAG 660
186 S   A   Y   P   L   Q   P   E   D   V   N   L   R   V   I   S   E   Y   Q   K 205
                670         680         690         700         710         720
                 .           .           .           .           .           .
661 CTC TTT CCT GAC ATT CCC ATA GGG TAT TCT GGG CAT GAA ACA GGC ATA GCG ATA TCT GTG 720
206 L   F   P   D   I   P   I   G   Y   S   G   H   E   T   G   I   A   I   S   V 225
                730         740         750         760         770         780
                 .           .           .           .           .           .
721 GCC GCA GTG GCT CTG GGG GCC AAG GTG TTG GAA CGT CAC ATA ACT TTG GAC AAG ACC TGG 780
226 A   A   V   A   L   G   A   K   V   L   E   R   H   I   T   L   D   K   T   W 245
                790         800         810         820         830         840
                 .           .           .           .           .           .
781 AAG GGG AGT GAC CAC TCG GCC TCG CTG GAG CCT GGA GAA CTG GCC GAG CTG GTG CGG TCA 840
246 K   G   S   D   H   S   A   S   L   E   P   G   E   L   A   E   L   V   R   S 265
                850         860         870         880         890         900
                 .           .           .           .           .           .
841 GTG CGT CTT GTG GAG CGT GCC CTG GGC TCC CCA ACC AAG CAG CTG CTG CCC TGT GAG ATG 900
266 V   R   L   V   E   R   A   L   G   S   P   T   K   Q   L   L   P   C   E   M 285
                910         920         930         940         950         960
                 .           .           .           .           .           .
901 GCC TGC AAT GAG AAG CTG GGC AAG TCT GTG GTG GCC AAA GTG AAA ATT CCG GAA GGC ACC 960
286 A   C   N   E   K   L   G   K   S   V   V   A   K   V   K   I   P   E   G   T 305
```

FIG. 35B

```
                970         980         990         1000        1010        1020
                .           .           .           .           .           .
961 ATT CTA ACA ATG GAC ATG CTC ACC GTG AAG GTG GGT GAG CCC AAA GCC TAT CCT CCT GAA 1020
306 I   L   T   M   D   M   L   T   V   K   V   G   E   P   K   A   Y   P   P   E 325
                1030        1040        1050        1060        1070        1080
                .           .           .           .           .           .
1021 GAC ATC TTT AAT CTA GTG GGC AAG AAG GTC CTG GTC ACT GTT GAA GAG GAT GAC ACC ATC 1080
326 D   I   F   N   L   V   G   K   K   V   L   V   T   V   E   E   D   D   T   I 345
                1090        1100        1110        1120        1130        1140
                .           .           .           .           .           .
1081 ATG GAA GAA TTG GTA GAT AAT CAT GGC AAA AAA ATC AAG TCT TAA AAA TAA AGT GCC ATT 1140
346 M   E   E   L   V   D   N   H   G   K   K   I   K   S   *                   359

1141 CTC TGA 1146
```

FIG. 35C

```
  1 MPLELELCPGRWVGGQHPCFIIAEIGQNHQGDLDVAKRMIRMAKECGADCAKFQKSELEF
    |                   | |||| || |  | |  ||  ||| |    |||
  1 MS---------------NIYIVAEIGCNHNGSVDIAREMILKAKEAGVNAVKFQTFKADK

 61 KFNRKALERPYTSKHSWG-KTYGEHKRHLEFSHDQYRELQRYAEEVGIFFTASGMDEMAV
        |   | |          |    ||   | |  |  ||            ||
 46 LISAIAPKAEYQIKNTGELESQLEMTKKLEMKYDDYLHLMEYAVSLNLDVFSTPFDEDSI

120 EFLHELNVPFFKVGSGDTNNFPYLEKTAK---KGRPMVISSGMQSMDTMKQ---VYQIVK
     ||  |     |  ||   | ||||| ||          || ||   |  ||        |
106 DFLASLKQKIWKIPSGELLNLPYLEKIAKLPIPDKKIIISTGMATIDEIKQSVSIFINNK

174 PLNPNFCFLQCTSAYPLQPEDVNLRVISEYQKLFPDIPIGYSGHETGIAISVAAVALGAK
        |   | |   ||   |||| |    | ||   || | |  |     ||| |
166 VPVGNITILHCNTEYPTPFEDVNLNAINDLKKHFPKNNIGFSDHSSGFYAAIAAVPYGIT

234 VLERHITLDKTWKGSDHSASLEPGELAELVRSVRLVERALGSPTKQLLPCEMACNEKLGK
     | | ||||   | || || || ||  |   || ||  |||  |     |        |
226 FIEKHFTLDKSMSGPDHLASIEPDELKHLCIGVRCVEKSLGSNSKVVTASERKNKIVARK

294 SVVAKVKIPEGTILTMDMLTVKVGEPKAYPPEDIFNLVGKKVLVTVEEDDTIMEELVDNH
    |  ||  |  |        | |        |    || ||       | | |  ||
286 SIIAKTEIKKGEVFSEKNITTKRP-GNGISPMEWYNLLGK-----IAEQDFIPDELIIHS

354 G-KKIKS
      |
340 EFKNQGE
```

FIG. 35D

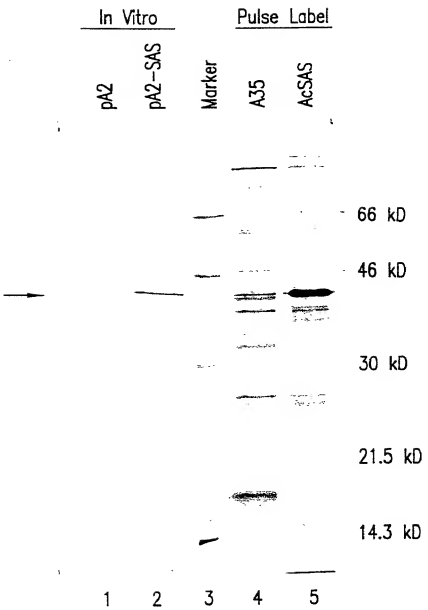

In Vitro
Pulse Label
pA2
pA2-SAS
Marker
A35
AcSAS
66 kD
46 kD
30 kD
21.5 kD
14.3 kD
1
2
3
4
5

FIG.36A

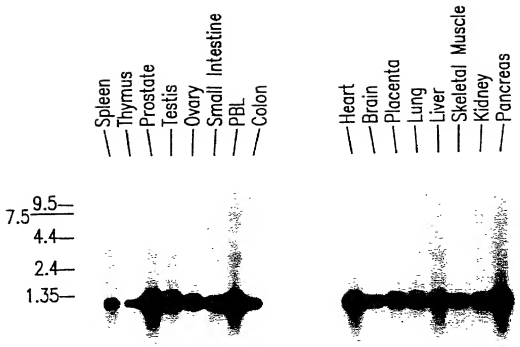

Spleen
Thymus
Prostate
Testis
Ovary
Small Intestine
PBL
Colon
Heart
Brain
Placenta
Lung
Liver
Skeletal Muscle
Kidney
Pancreas
9.5
7.5
4.4
2.4
1.35

FIG.36B

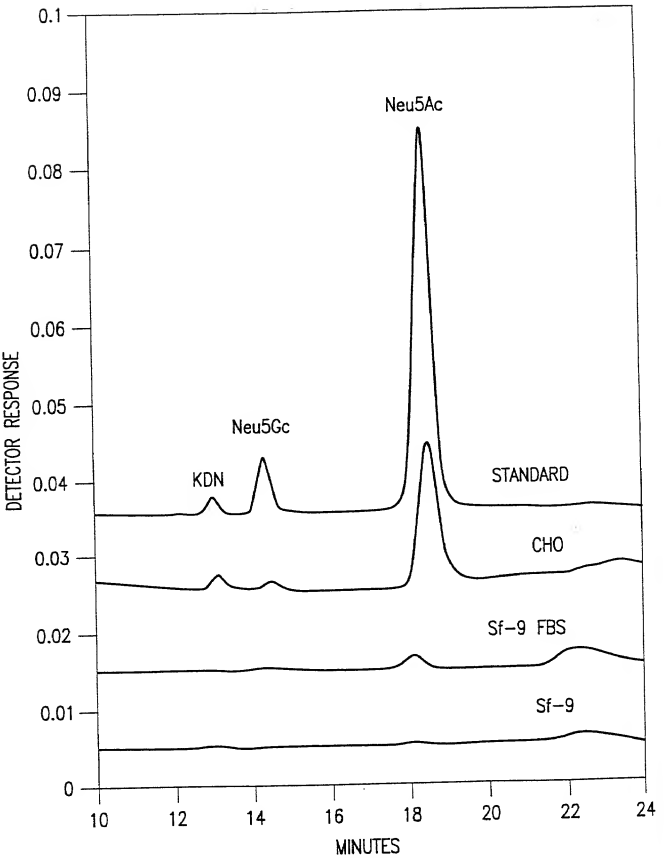

0.1
0.09
0.08
0.07
0.06
0.05
0.04
0.03
0.02
0.01
0
DETECTOR RESPONSE
Neu5Ac
Neu5Gc
KDN
STANDARD
CHO
Sf−9 FBS
Sf−9
10
12
14
16
18
20
22
24
MINUTES

FIG. 37A

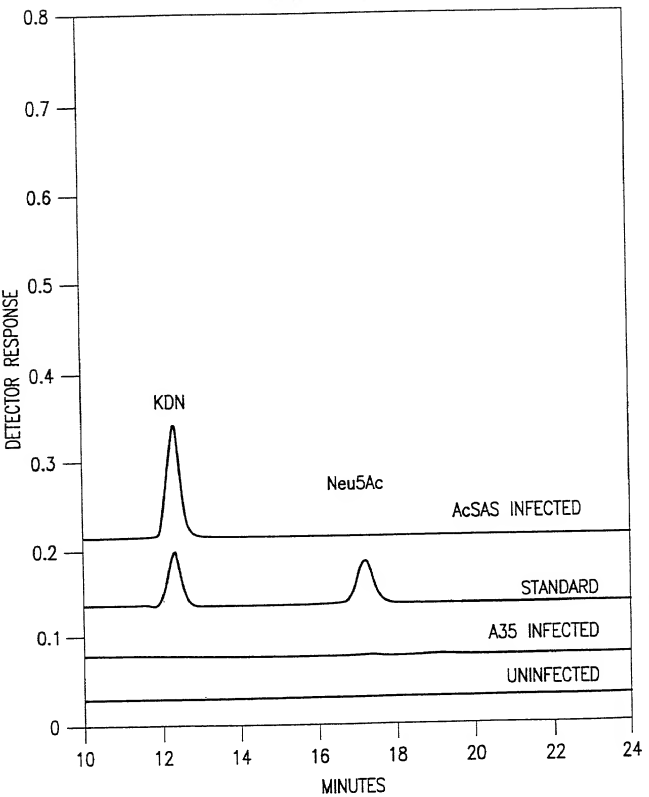

0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
DETECTOR RESPONSE
KDN
Neu5Ac
AcSAS INFECTED
STANDARD
A35 INFECTED
UNINFECTED
10
12
14
16
18
20
22
24
MINUTES

FIG. 37B

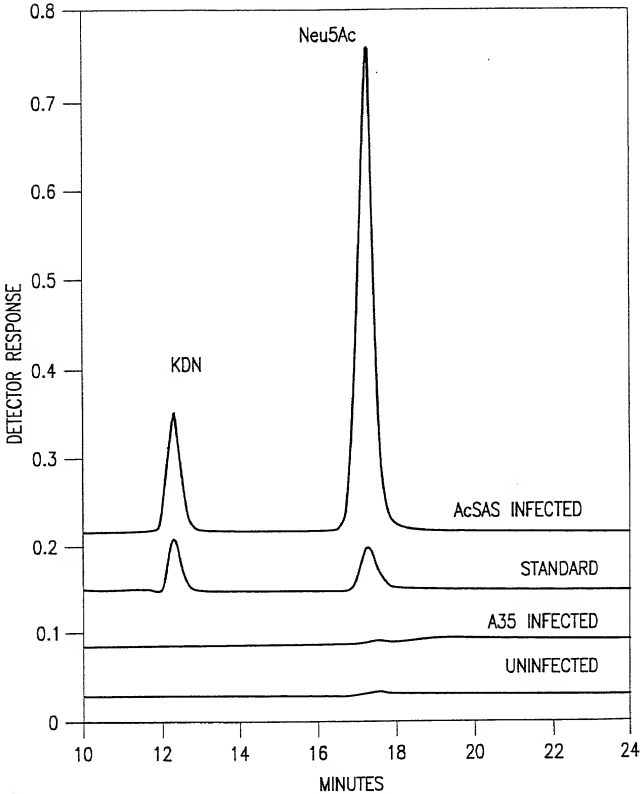

0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
DETECTOR RESPONSE
Neu5Ac
KDN
AcSAS INFECTED
STANDARD
A35 INFECTED
UNINFECTED
10
12
14
16
18
20
22
24
MINUTES

FIG. 37C

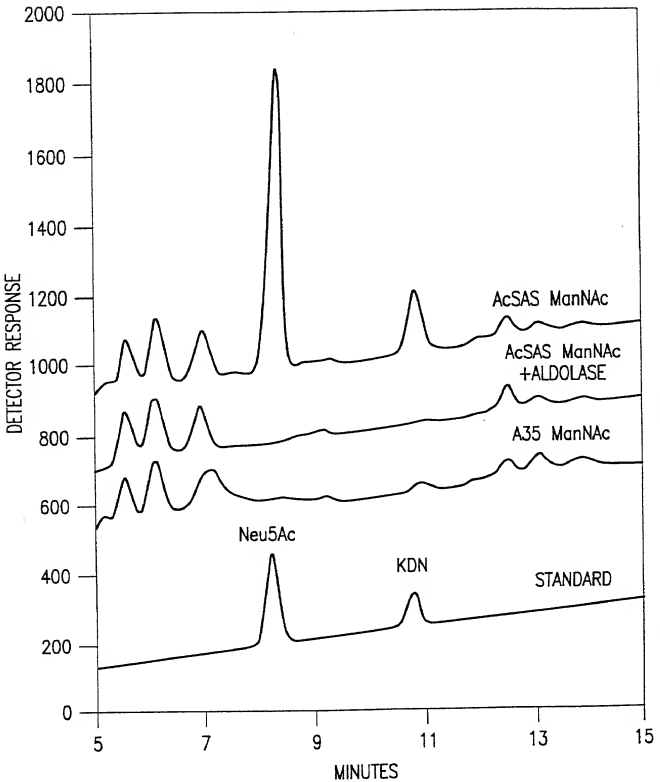

2000
1800
1600
1400
1200
1000
800
600
400
200
0
DETECTOR RESPONSE
AcSAS ManNAc
AcSAS ManNAc
+ALDOLASE
A35 ManNAc
Neu5Ac
KDN
STANDARD
5
7
9
11
13
15
MINUTES

FIG. 37D

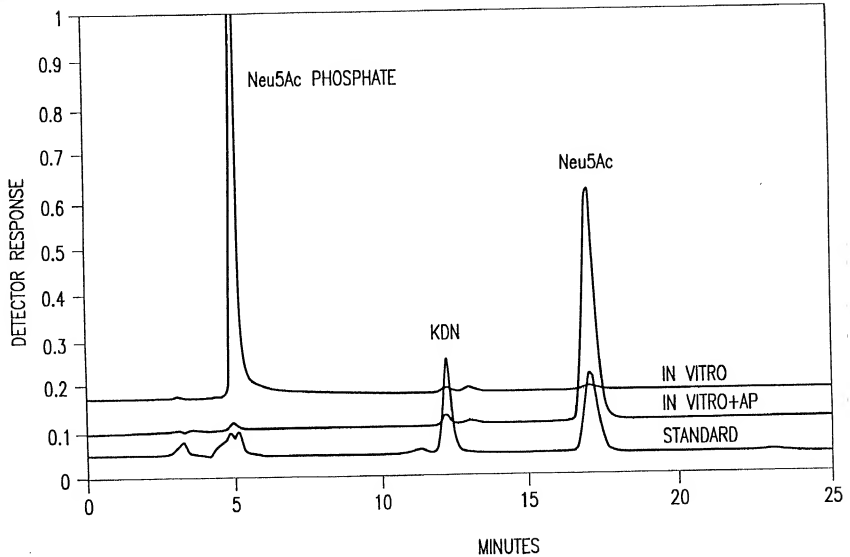


FIG. 38A

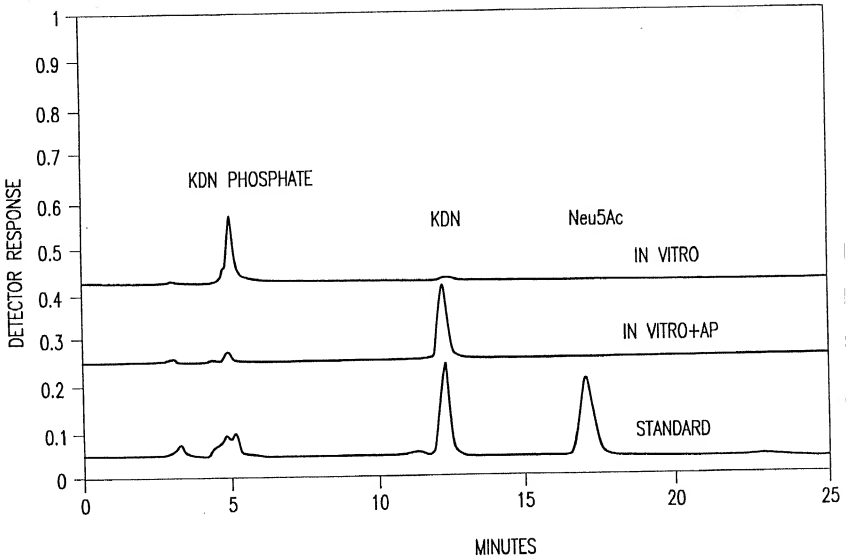


FIG. 38B

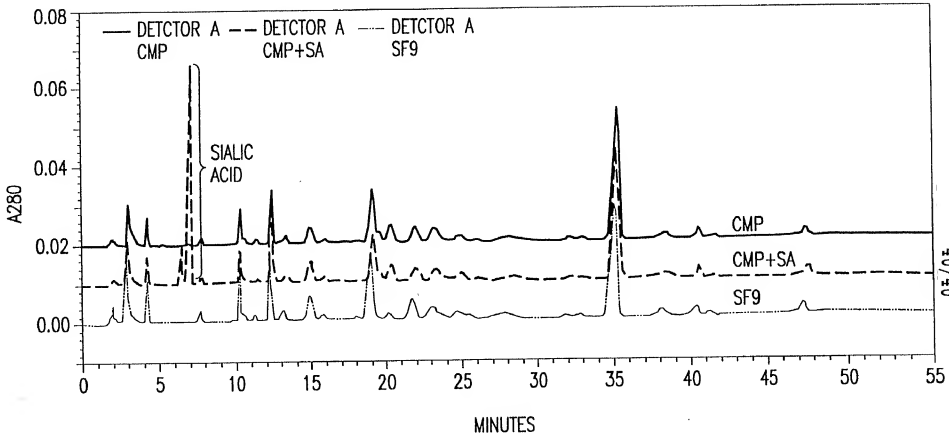


FIG. 39